

ID U79117 standard; DNA; PRO; 3573 BP.
 XX
 AC U79117;
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 SV U79117.1
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 DT 04-SEP-1998 (Rel. 56, Created)
 DT 04-SEP-1998 (Rel. 56, Last updated, Version 1)
 XX
 DE Clostridium thermocellum S-layer protein (slpA) gene, complete cds.
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 KW .
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 OS Clostridium thermocellum
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
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 RN [1]
 RP 1-3573
 RX MEDLINE; 98129094.
 RA Lemaire M., Miras I., Gounon P., Beguin P.;
 RT "Identification of a region responsible for binding to the cell wall within
 RT the S-layer protein of Clostridium thermocellum";
 RL Microbiology 144(Pt):0-0(0).
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 RN [2]
 RP 1-3573
 RA Miras I., Beguin P.;
 RT ;
 RL Submitted (20-NOV-1996) to the EMBL/GenBank/DDBJ databases.
 RL Biotechnology, Institut Pasteur, 28, rue du Dr. Roux, Paris 75724 Cedex 15,
 RL France
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 DR SPTREMBL; 086999; 086999.
 XX

Key	Location/Qualifiers
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Entry information

Entry name	O86999
Primary accession number	O86999
Secondary accession numbers	None
Entered in TrEMBL in	Release 08, November 1998
Sequence was last modified in	Release 08, November 1998
Annotations were last modified in	Release 24, June 2003

Name and origin of the protein

Protein name	S-layer protein
Synonyms	None
Gene name	SLPA
From	<u>Clostridium thermocellum</u> [TaxID: <u>1515</u>]
Taxonomy	<u>Bacteria</u> ; <u>Firmicutes</u> ; <u>Clostridia</u> ; <u>Clostridiales</u> ; <u>Clostridiaceae</u> ; <u>Clostridium</u> .

References

- [1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=NCIB 10682;
MEDLINE=98129094; PubMed=9467913; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]
[Lemaire M.](#), [Miras I.](#), [Gounon P.](#), [Beguin P.](#);
 "Identification of a region responsible for binding to the cell wall within the S-layer protein of Clostridium thermocellum.";
 Microbiology 144:0-0(0).

Comments

None

Cross-references

EMBL	U79117; AAC33404.1; [EMBL / GenBank / DDBJ] -. [CoDingSequence]
PIR	T30311; T30311.
InterPro	IPR001119 ; SLH. Graphical view of domain structure.
Pfam	PF00395 ; SLH; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
ProtoMap	O86999 .
PRESAGE	O86999 .
ModBase	O86999 .
SWISS-2DPAGE	Get region on 2D PAGE.

Keywords

None

Features

None

Sequence information

Length: 1036 AA	Molecular weight: 113330 Da	CRC64: 1AF2202060D7C2A1 [This is a checksum on the sequence]
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[Dotlet \(Java\)](#)



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ID AY004256 standard; DNA; PRO; 2434 BP.
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 SV AY004256.1
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 DT 10-APR-2001 (Rel. 67, Last updated, Version 3)
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 RP 1-2434
 RX MEDLINE; 21189268.
 RX PUBMED; 11292772.
 RA Karjalainen T.K., Waligora-Dupriet A.J., Cerquetti M., Spigaglia P.,
 RA Mauri P., Mastrantonio P.;
 RT "Molecular and genomic analysis of two genes encoding surface-anchored
 RT proteins from Clostridium difficile";
 RL Infect. Immun. 69(5):3442-3446 (2001).
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 RN [2]
 RP 1-2434
 RA Karjalainen T.K.;
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 RL Submitted (05-JUL-2000) to the EMBL/GenBank/DDBJ databases.
 RL Microbiology, Univ Paris-Sud, Faculty of Pharmacy, 5, rue JB Clement,
 RL Chatenay-Malabry 92296, France
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 DR SPTREMBL; Q9EY85; Q9EY85.
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aaaaagatgt	ttaattttatt	taagtaaaat	cattatacta	taaatcaaaa	taattgtcta	2400
ctattatgga	tttttaattgt	ataatagtaa	ttgg			2434

//

WEST Search History

DATE: Tuesday, August 12, 2003

Set Name Query

side by side

Hit Count Set Name

result set

DB=USPT; PLUR=YES; OP=AND

L1 difficile.clm. same (vaccin\$ or pharmaceu\$
or therapeut\$).clm.

17 L1

END OF SEARCH HISTORY

WEST

Generate Collection

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L1: Entry 15 of 17

File: USPT

Nov 14, 1995

DOCUMENT-IDENTIFIER: US 5466672 A

TITLE: Therapeutic use of clostridium difficile toxin A

CLAIMS:

5. A method of treating cancer, comprising:

- a) providing i) a patient with gastrointestinal cancer, and ii) a preparation comprising Clostridium difficile toxin A in an aqueous solution in therapeutic amounts that is intravenously injectable; and
- b) intravenously injecting said toxin into said patient.

WEST

Generate Collection

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L1: Entry 9 of 17

File: USPT

Jun 27, 2000

DOCUMENT-IDENTIFIER: US 6080725 A

TITLE: Immunostimulating and vaccine compositions employing saponin analog adjuvants and uses thereof

CLAIMS:

12. The vaccine of claim 11, wherein said bacterial antigens are antigens associated with a bacterium selected from the group consisting of *Helicobacter pylori*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Ureaplasma urealyticum*, *Mycoplasma pneumoniae*, *Staphylococcus* spp., *Staphylococcus aureus*, *Streptococcus* spp., *Streptococcus pyogenes*, *Streptococcus pneumoniae*, *Streptococcus viridans*, *Enterococcus faecalis*, *Neisseria meningitidis*, *Neisseria gonorrhoeae*, *Bacillus anthracis*, *Salmonella* spp., *Salmonella typhi*, *Vibrio cholera*, *Pasteurella pestis*, *Pseudomonas aeruginosa*, *Campylobacter* spp., *Campylobacter jejuni*, *Clostridium* spp., *Clostridium difficile*, *Mycobacterium* spp., *Mycobacterium tuberculosis*, *Treponema* spp., *Borrelia* spp., *Borrelia burgdorferi*, *Leptospria* spp., *Hemophilus ducreyi*, *Corynebacterium diphtheria*, *Bordetella pertussis*, *Bordetella parapertussis*, *Bordetella bronchiseptica*, *hemophilus influenza*, *Escherichia coli*, *Shigella* spp., *Erlichia* spp., *Rickettsia* spp. and combinations thereof.

WEST

Generate Collection

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L1: Entry 7 of 17

File: USPT


Jul 17, 2001

DOCUMENT-IDENTIFIER: US 6262029 B1

TITLE: Chemically modified saponins and the use thereof as adjuvants

CLAIMS:

29. The vaccine of claim 28, wherein said bacterial antigens are antigens associated with a bacterium selected from the group consisting of *Helicobacter pylori*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Ureaplasma urealyticum*, *Mycoplasma pneumoniae*, *Staphylococcus* spp., *Staphylococcus aureus*, *Streptococcus* spp., *Streptococcus pyogenes*, *Streptococcus pneumoniae*, *Streptococcus viridans*, *Enterococcus faecalis*, *Neisseria meningitidis*, *Neisseria gonorrhoeae*, *Bacillus anthracis*, *Salmonella* spp., *Salmonella typhi*, *Vibrio cholera*, *Pasteurella pestis*, *Pseudomonas aeruginosa*, *Campylobacter* spp., *Campylobacter jejuni*, *Clostridium* spp., *Clostridium difficile*, *Mycobacterium* spp., *Mycobacterium tuberculosis*, *Treponema* spp., *Borrelia* spp., *Borrelia burgdorferi*, *Leptospria* spp., *Hemophilus ducreyi*, *Corynebacterium diphtheria*, *Bordetella pertussis*, *Bordetella parapertussis*, *Bordetella bronchiseptica*, *hemophilus influenza*, *Escherichia coli*, *Shigella* spp., *Erlichia* spp., *Rickettsia* spp. and combinations thereof.

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[\[Keywords\]](#) [\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)

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Entry information

Entry name	Q8KHB6
Primary accession number	Q8KHB6
Secondary accession numbers	None
Entered in TrEMBL in	Release 22, October 2002
Sequence was last modified in	Release 22, October 2002
Annotations were last modified in	Release 22, October 2002

Name and origin of the protein

Protein name	S-layer protein variable domain SlpA [Fragment]
Synonyms	None
Gene name	SLPA
From	<u>Clostridium difficile</u> [TaxID: 1496]
Taxonomy	<u>Bacteria</u> ; <u>Firmicutes</u> ; <u>Clostridia</u> ; <u>Clostridiales</u> ; <u>Clostridiaceae</u> ; <u>Clostridium</u> .

References

- [1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=ATCC 43597, 90-111, and 93-136;
MEDLINE=22083941; PubMed=12089261; [NCBI, ExPASy, EBI, Israel,
Japan]
Karjalainen T., Saumier N., Barc M.C., Delmee M., Collignon A.;
"Clostridium difficile Genotyping Based on slpA Variable Region in S-Layer
Gene Sequence: an Alternative to Serotyping."
J. Clin. Microbiol. 40:2452-2458(2002).

Comments

None

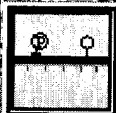
Cross-references

EMBL	AF458880;	[EMBL / GenBank / DDBJ]
	AAM75944.1; -.	[CoDingSequence]
	AF458881;	[EMBL / GenBank / DDBJ]
	AAM75945.1; -.	[CoDingSequence]
	AF458882;	[EMBL / GenBank / DDBJ]
	AAM75946.1; -.	[CoDingSequence]
HOBACGEN	[Family / Alignment / Tree]	
ProtoMap	Q8KHB6 .	
PRESAGE	Q8KHB6 .	
ModBase	Q8KHB6 .	
SWISS-2DPAGE	Get region on 2D PAGE .	

Keywords

None

Features



Feature table viewer

Key	From	To	Length	Description
NON_TER	1	1		
NON_TER	389	389		

Sequence information

Length: 389 AA [This is the length of the partial sequence]	Molecular weight: 41788 Da [This is the MW of the partial sequence]	CRC64: C5ED8F4901C18F8C [This is a checksum on the sequence]
---	---	---

10	20	30	40	50	60
AAPVFAATTP	SEDNAGKYTV	VKDKYKDIFD	EVKKLVKEND	AAIDAYLKEN	NSTDRDAAWT
70	80	90	100	110	120
ALAGTNSLNI	INITVKDSDD	DSVVVPKTVV	KTNTVVDTDY	VENKLNLDL	DEYVDFDITT
130	140	150	160	170	180
KASTVSSTKY	TAANIYDLAA	NNGKIIIDAL	KNVTEKQLKD	GGILGEVAKT	ISGATTPSAP
190	200	210	220	230	240
TGDTFASYFT	VGTVKTVNGK	VALEINIAEP	ASTVLVKTD	ELTTSPTTQQ	KMSFANAKIT
250	260	270	280	290	300
LTEGDDRLDF	SKPSIVDGAL	GDFAKAAATT	TPGKQQTINV	RVINAKQETV	KATDYDALK
310	320	330	340	350	360
VVSKYKFDST	EIGRVYDEAK	DLNDKDKLDG	SSYDKDGT	AVFFAEGKRL	QGFSSYGKFS
370	380				
TDEAESGLAD	GNAALKLVIE	STDEDDFID			

Q8KHB6 in
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[PeptideMass](#), [PeptideCutter](#),
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Entry information

Entry name	Q8KHH9
Primary accession number	Q8KHH9
Secondary accession numbers	None
Entered in TrEMBL in	Release 22, October 2002
Sequence was last modified in	Release 22, October 2002
Annotations were last modified in	Release 22, October 2002

Name and origin of the protein

Protein name	S-layer protein variable domain SlpA [Fragment]
Synonyms	None
Gene name	SLPA
From	<u>Clostridium difficile</u> [TaxID: 1496]
Taxonomy	<u>Bacteria</u> ; <u>Firmicutes</u> ; <u>Clostridia</u> ; <u>Clostridiales</u> ; <u>Clostridiaceae</u> ; <u>Clostridium</u> .

References

- [1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=56026, 54823, and ATCC 43601;
MEDLINE=22083941; PubMed=12089261; [NCBI, ExPASy, EBI, Israel,
Japan]
Karjalainen T., Saumier N., Barc M.C., Delmee M., Collignon A.;
"Clostridium difficile Genotyping Based on slpA Variable Region in S-Layer
Gene Sequence: an Alternative to Serotyping."
J. Clin. Microbiol. 40:2452-2458(2002).

Comments

None

Cross-references

EMBL	AF458884;	[EMBL / GenBank / DDBJ]
	AAM75939.1; -.	[CoDingSequence]
	AF458885;	[EMBL / GenBank / DDBJ]
	AAM75940.1; -.	[CoDingSequence]
	AF458883;	[EMBL / GenBank / DDBJ]
	AAM75947.1; -.	[CoDingSequence]
HOBACGEN	[Family / Alignment / Tree]	
ProtoMap	Q8KHH9 .	
PRESAGE	Q8KHH9 .	
ModBase	Q8KHH9 .	
SWISS-2DPAGE	Get region on 2D PAGE .	

Keywords

None

Features



Feature table viewer

Key	From	To	Length	Description
NON_TER	1	1		
NON_TER	339	339		

Sequence information

Length: 339 AA [This is the length of the partial sequence]	Molecular weight: 36205 Da [This is the MW of the partial sequence]	CRC64: 9FDB0B05COFFAA61 [This is a checksum on the sequence]
--	--	--

10	20	30	40	50	60
AAPVFANVVT	GSEGYTVSQK	DYKKAVKQIQ	DGIKKNIITS	INIYFDGTKV	STVNVAGDQD
70	80	90	100	110	120
ARDKIADDFN	NTVEGKLDL	GDGKYVDFEI	SYNKGVEEYT	KTELENYKKL	LDNKVVIPKA
130	140	150	160	170	180
SGVNP GAVKE	KSGSADEAVA	ADNDIKGSDL	YNTTVEADTT	NGGYKLSITA	KTISDVKYGT
190	200	210	220	230	240
IGAGKYPDAK	VITATGTDAL	VKGKTVDISA	SYALEASTGN	VSGLSLTDTN	PSSDSVNVRI
250	260	270	280	290	300
INAKEITIDL	DASSYDSAES	LAKKYVFKPS	TLTSIYTDIE	AGNIERVNGK	YQVEIFADGK
310	320	330			
RLNTLSAVNS	TIADPDSTAK	VIIKADKLKD	LKDYVDDLK		

Q8KHH9 in
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[\[Features\]](#)
[\[Sequence\]](#)
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Entry information	
Entry name	Q8KHI4
Primary accession number	Q8KHI4
Secondary accession numbers	None
Entered in TrEMBL in	Release 22, October 2002
Sequence was last modified in	Release 22, October 2002
Annotations were last modified in	Release 22, October 2002
Name and origin of the protein	
Protein name	S-layer protein [Fragment]
Synonyms	None
Gene name	SLPA
From	<u>Clostridium difficile</u> [TaxID: 1496]
Taxonomy	<u>Bacteria</u> ; <u>Firmicutes</u> ; <u>Clostridia</u> ; <u>Clostridiales</u> ; <u>Clostridiaceae</u> ; <u>Clostridium</u> .

References

- [1] SEQUENCE FROM NUCLEIC ACID.
 STRAIN=ATCC 43598, GAI95600, and GAI95601;
 MEDLINE=22083941; PubMed=12089261; [[NCBI](#), [ExpASY](#), [EBI](#), [Israel](#), [Japan](#)]
[Karjalainen T.](#), [Saumier N.](#), [Barc M.C.](#), [Delmee M.](#), [Collignon A.](#);
 "Clostridium difficile Genotyping Based on slpA Variable Region in S-Layer
 Gene Sequence: an Alternative to Serotyping."
 J. Clin. Microbiol. 40:2452-2458(2002).

Comments

None

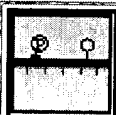
Cross-references

EMBL	AF448125;	[EMBL / GenBank / DDBJ]
	AAM75925.1; -.	[CoDingSequence]
	AF448126;	[EMBL / GenBank / DDBJ]
	AAM75926.1; -.	[CoDingSequence]
	AF448127;	[EMBL / GenBank / DDBJ]
	AAM75927.1; -.	[CoDingSequence]
HOBACGEN	[Family / Alignment / Tree]	
ProtoMap	Q8KHI4 .	
PRESAGE	Q8KHI4 .	
ModBase	Q8KHI4 .	
SWISS-2DPAGE	Get region on 2D PAGE .	

Keywords

None

Features



[Feature table viewer](#)

Key	From	To	Length	Description
NON_TER	1	1		
NON_TER	354	354		

Sequence information

Length: 354 AA
 [This is the length
 of the partial
 sequence]

Molecular weight:
37738 Da [This is the
 MW of the partial
 sequence]

CRC64: 9D558CDF0B136E10
 [This is a checksum on the
 sequence]

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AAPIFADSTT	PGYTVVKNDW	KKAVKQLQDG	LKNKTISTIK	VSFNGNSVGE	VTPASSGAKK
70	80	90	100	110	120
ADRDAAAEKL	YNLVNTQLDK	LGDGDYVDFE	VTYNLATQII	TKAEAEAVLT	KLQQYNDKVL
130	140	150	160	170	180
INSATDTVKG	MVSDTQVDSK	NVAANPLKVS	DMYTIPSAIT	GSDDSGYSIA	KPTEKTTSL
190	200	210	220	230	240
YGTVGDATA	GKAITVDTASN	EAFAGNGKVI	DYNKSFKATV	QGDGTVKTS	G VVLKDASDMA
250	260	270	280	290	300
ATGTIKVRVT	SAKEESIDVD	SSSYISAENL	AKKYVFNPKE	VSEAYNAIVA	LQNDGIESDL
310	320	330	340	350	
VQLVNGKYQV	IFYPEGKRLE	TKSADIADA	DSPAKITIKA	NKLKDLKDYV	DDLK

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